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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/894,749

DATE: 07/20/2001  
 TIME: 11:25:14

Input Set : N:\Crf3\RULE60\09894749.txt  
 Output Set: N:\CRF3\07202001\I894749.raw

5 <110> APPLICANT: Hodge, Martin R.  
 7 Yowe, David  
 11 <120> TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof  
 15 <130> FILE REFERENCE: 5800-19, 035800/174680  
 19 <140> CURRENT APPLICATION NUMBER: 09/894,749  
 21 <141> CURRENT FILING DATE: 2001-06-27  
 23 <150> PRIOR APPLICATION NUMBER: 09/244,314  
 25 <151> PRIOR FILING DATE: 1999-02-04  
 27 <160> NUMBER OF SEQ ID NOS: 4  
 31 <170> SOFTWARE: PatentIn Ver. 2.0  
 35 <210> SEQ ID NO: 1  
 37 <211> LENGTH: 2217  
 39 <212> TYPE: DNA  
 41 <213> ORGANISM: Homo sapiens  
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 47 <221> NAME/KEY: CDS  
 49 <222> LOCATION: (160)..(867)  
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 63 gatgtataaa attagacatc tottcatttt agagagaag atg gaa aca aca ttg 174  
 65 Met Glu Thr Thr Leu  
 67 1 5  
 71 ctt ttc ttt tct caa ata aat atg tgt gaa tca aaa gaa aaa act ttt 222  
 73 Leu Phe Phe Ser Gln Ile Asn Met Cys Glu Ser Lys Glu Lys Thr Phe  
 75 10 15 20  
 79 ttc aag tta ata cat ggt tca gga aaa gaa aca agc aaa gaa gcc 270  
 81 Phe Lys Leu Ile His Gly Ser Gly Lys Glu Glu Thr Ser Lys Glu Ala  
 83 25 30 35  
 87 aaa atc aga gct aag gaa aaa aga aat aga cta agt ctt ctt gtg cag 318  
 89 Lys Ile Arg Ala Lys Glu Lys Arg Asn Arg Leu Ser Leu Leu Val Gln  
 91 40 45 50  
 95 aaa cct gag ttt cat gaa gac acc cgc tcc agt aga tct ggg cac ttg 366  
 97 Lys Pro Glu Phe His Glu Asp Thr Arg Ser Ser Arg Ser Gly His Leu  
 99 55 60 65  
 103 gcc aaa gaa aca aga gtc tcc cct gaa gag gca gtg aaa tgg ggt gaa 414  
 105 Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala Val Lys Trp Gly Glu  
 107 70 75 80 85  
 111 tca ttt gac aaa ctg ctt tcc cat aga gat gga cta gag gct ttt acc 462  
 113 Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly Leu Glu Ala Phe Thr  
 115 90 95 100  
 119 aga ttt ctt aaa act gaa ttc agt gaa gaa aat att gaa ttt tgg ata 510  
 121 Arg Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Ile Glu Phe Trp Ile  
 123 105 110 115  
 127 gcc tgt gaa gat ttc aag aaa agc aag gga cct caa caa att cac ctt 558  
 129 Ala Cys Glu Asp Phe Lys Lys Ser Lys Gly Pro Gln Gln Ile His Leu  
 131 120 125 130

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143	gag gtt aac ctt gat ttt cac	aca aaa gaa gtc att aca aac	agc atc	654			
145	Glu Val Asn Leu Asp Phe His	Thr Lys Glu Val Ile Thr Asn Ser Ile					
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151	actcaa cct acc ctc cac agt	ttt gat gct gca caa	agc aga gtg tat	702			
153	Thr Gln Pro Thr Leu His Ser Phe Asp Ala Ala	Gln Ser Arg Val Tyr					
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159	cag ctc atg gaa caa gac	agt tat aca cgt ttt ctg aaa	tct gac atc	750			
161	Gln Leu Met Glu Gln Asp Ser Tyr	Thr Arg Phe Leu Lys Ser Asp Ile					
163	185	190	195				
167	tat tta gac ttg atg gaa gga	aga cct cag aga cca aca aat	ctt agg	798			
169	Tyr Leu Asp Leu Met Glu Gly Arg Pro Gln Arg Pro	Thr Asn Leu Arg					
171	200	205	210				
175	aga cga tca cgc tca ttt acc	tgc aat gaa ttc caa	gat gta caa tca	846			
177	Arg Arg Ser Arg Ser Phe Thr Cys Asn Glu Phe Gln Asp Val Gln Ser						
179	215	220	225				
183	gat gtt gcc att tgg tta taa	agaaaaattga	ttttgctcat ttttatgaca	897			
185	Asp Val Ala Ile Trp Leu						
187	230	235					
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199	aaaatacata cagtatctgc	cagtatattc	tgtaaaaacct tctatttgat	1077			
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211	acaaaagtct agttgggatt	ttttacccaa	gcagcataat	atgtgttata	taaacataat	1257	
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223	gttactacta accctgtccc	aagaatagta	atatcacctc	tagttataag	ccagcaacag	1437	
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239	ggaactaagt agactacott	atcaccggct	aagaaaactt	gctactaaac	tattaggcca	1677	
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247	tagaattggg gtagaaatca	gaaatgagat	gaggggaaga	agcaaggagt	ctaaggccct	1797	
251	agcgatttgg	gcatctgcca	cattggttca	tattcagaaa	gtgttatctc	attgattata	1857
255	ttcttgtaa	gcaaactc	ttaagtaatt	attattcaaa	taagattata	ctcatacatc	1917
259	tatatgtcac	tgtttaaag	agatatttaa	ttttatgt	gtgttacatg	gtctgtaaat	1977
263	atttgttattt	aaaaatgcca	tgcatttaggc	tttggaaatt	taatgttagt	tgaaatgtaa	2037
267	aatgtgaaaa	ctttagatca	ttttagttaa	taaatatttt	taacttcatt	catacagtt	2097
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283	<211> LENGTH: 235						
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287	<213> ORGANISM: Homo sapiens						
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295	1	5	10	15
299	Lys Glu Lys Thr Phe Phe Lys Leu Ile His Gly Ser Gly Lys Glu Glu			
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305	Thr Ser Lys Glu Ala Lys Ile Arg Ala Lys Glu Lys Arg Asn Arg Leu			
307	35	40	45	
311	Ser Leu Leu Val Gln Lys Pro Glu Phe His Glu Asp Thr Arg Ser Ser			
313	50	55	60	
317	Arg Ser Gly His Leu Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala			
319	65	70	75	80
323	Val Lys Trp Gly Glu Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly			
325	85	90	95	
329	Leu Glu Ala Phe Thr Arg Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn			
331	100	105	110	
335	Ile Glu Phe Trp Ile Ala Cys Glu Asp Phe Lys Ser Lys Gly Pro			
337	115	120	125	
341	Gln Gln Ile His Leu Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln			
343	130	135	140	
347	Thr Asp Ala Pro Lys Glu Val Asn Leu Asp Phe His Thr Lys Glu Val			
349	145	150	155	160
353	Ile Thr Asn Ser Ile Thr Gln Pro Thr Leu His Ser Phe Asp Ala Ala			
355	165	170	175	
359	Gln Ser Arg Val Tyr Gln Leu Met Glu Gln Asp Ser Tyr Thr Arg Phe			
361	180	185	190	
365	Leu Lys Ser Asp Ile Tyr Leu Asp Leu Met Glu Gly Arg Pro Gln Arg			
367	195	200	205	
371	Pro Thr Asn Leu Arg Arg Ser Arg Ser Phe Thr Cys Asn Glu Phe			
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413	actggacag aat atg gat atg tca ctg gtt ttc tct caa tta aat 169			
415	Met Asp Met Ser Leu Val Phe Phe Ser Gln Leu Asn			
417	1	5	10	
421	atg tgt gaa tca aaa gag aaa act ttt ttc aaa cta atg cat ggg tca 217			
423	Met Cys Glu Ser Lys Glu Lys Thr Phe Phe Lys Leu Met His Gly Ser			
425	15	20	25	
429	ggg aaa gaa gaa aca agc atc gag gcc aaa atc aga gcg aaa gaa aaa 265			
431	Gly Lys Glu Glu Thr Ser Ile Glu Ala Lys Ile Arg Ala Lys Glu Lys			
433	30	35	40	
437	agg aat aga cta agt ctt ctc cta cag agg cct gac ttc cat gga gag 313			

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441 45 50 55 60
445 act caa gcc agt aga tct gcc ctc ttg gcc aaa gaa aca aga gtc tct 361
447 Thr Gln Ala Ser Arg Ser Ala Leu Leu Ala Lys Glu Thr Arg Val Ser
449 65 70 75
453 cct gaa gaa gca gtg aaa tgg gct gaa tca ttt gac aaa ttg ctc tct 409
455 Pro Glu Glu Ala Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu Ser
457 80 85 90
461 cat aga gat gga gtg gat gct ttt acc aga ttt ctt aaa act gaa ttc 457
463 His Arg Asp Gly Val Asp Ala Phe Thr Arg Phe Leu Lys Thr Glu Phe
465 95 100 105
469 agt gag gag aac att gaa ttt tgg gtc gcc tgt gaa gac ttc aag aaa 505
471 Ser Glu Glu Asn Ile Glu Phe Trp Val Ala Cys Glu Asp Phe Lys Lys
473 110 115 120
477 tgc aag gaa cct caa caa atc atc cta aaa gca aag gca atc tat gag 553
479 Cys Lys Glu Pro Gln Gln Ile Ile Leu Lys Ala Lys Ala Ile Tyr Glu
481 125 130 135 140
485 aaa ttc att cag aat gat gcc ccc aaa gag gtt aac att gat ttt cat 601
487 Lys Phe Ile Gln Asn Asp Ala Pro Lys Glu Val Asn Ile Asp Phe His
489 145 150 155
493 act aaa gaa gta att gct aag agc atc gcc cag ccc act ctc cac agt 649
495 Thr Lys Glu Val Ile Ala Lys Ser Ile Ala Gln Pro Thr Leu His Ser
497 160 165 170
501 ttt gat acg gca caa agc aga gtg tac cag ctc atg gaa cat gac agt 697
503 Phe Asp Thr Ala Gln Ser Arg Val Tyr Gln Leu Met Glu His Asp Ser
505 175 180 185
509 tat aaa cgc ttt ttg aaa tct gag acc tac tta cat ttg ata gaa gga 745
511 Tyr Lys Arg Phe Leu Lys Ser Glu Thr Tyr Leu His Leu Ile Glu Gly
513 190 195 200
517 aga cct cag aga cca aca aac ctt agg aga cga tca cga tca ttt act 793
519 Arg Pro Gln Arg Pro Thr Asn Leu Arg Arg Arg Ser Arg Ser Phe Thr
521 205 210 215 220
525 tac aat gat ttc caa gat gta aag tca gat gtt gcc att tgg tta tga 841
527 Tyr Asn Asp Phe Gln Asp Val Lys Ser Asp Val Ala Ile Trp Leu
529 225 230 235
533 gtaaaaagtca tttgtcttct ttgtatagg tatgtgtata tctaaaatat atactaatac 901
537 taatgtgtac ttctaaaata tagtttgtt ataagaagag atgatttcat ttttaaaaata 961
541 caccatgcaa atacatatta aatgtaaagaa ctttttatat tatactaaaa taattcatca 1021
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561 <211> LENGTH: 235
563 <212> TYPE: PRT
565 <213> ORGANISM: Mus sp.
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## RAW SEQUENCE LISTING

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Input Set : N:\Crf3\RELEAS\09894749.txt  
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595	Arg Ser Ala Leu Leu Ala Lys Glu Thr Arg Val	Ser Pro Glu Glu Ala
597	65	70
601	Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu	Ser His Arg Asp Gly
603	85	90
607	Val Asp Ala Phe Thr Arg Phe Leu Lys	Thr Ser Glu Glu Asn
609	100	105
613	Ile Glu Phe Trp Val Ala Cys	Cys Asp Phe Lys Lys Cys Lys Glu Pro
615	115	120
619	Gln Gln Ile Ile Leu	Lys Ala Ile Tyr Glu Lys Phe Ile Gln
621	130	135
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627	145	150
631	Ile Ala Lys Ser Ile Ala Gln Pro Thr Leu His	Ser Phe Asp Thr Ala
633	165	170
637	Gln Ser Arg Val Tyr Gln Leu Met Glu His Asp Ser	Tyr Lys Arg Phe
639	180	185
643	Leu Lys Ser Glu Thr Tyr Leu His Leu Ile Glu	Gly Arg Pro Gln Arg
645	195	200
649	Pro Thr Asn Leu Arg Arg Ser Arg Ser Phe	Thr Tyr Asn Asp Phe
651	210	215
655	Gln Asp Val Lys Ser Asp Val Ala Ile Trp Leu	
657	225	230
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**VERIFICATION SUMMARY**

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